## Please replace the paragraphs on page 44, lines 8-24 with the following paragraphs:

The glycosylation site was next removed by replacing the region from a unique *Xcm*I site to a unique *Sph*I site within the BPI gene in pSS101 with an annealed oligonucleotide that contained the codon (TCC) for the serine at amino acid position 351 changed to the codon (GCC) for alanine as shown below.

```
Wild type

XcmI

...CCC AAC TCC TCC CTG GCT TCC CTC TTC CTG ATT GGC ATG CAC (SEQ ID NO:9)

...GGG TTC AGG AGG GAC CGA AGG GAG AAG GAC TAA CCG TAC GTG (SEQ ID NO:10)

Pro Asn Ser Ser Leu Ala Ser Leu Phe Leu Ile GlyMet His (SEQ ID NO:11)

351

Nonglycosylated

XcmI

...CCC AAC TCC GCC CTG GCT TCC CTC TTC CTG ATT GGC ATG CAC (SEQ ID NO:12)

...GGG TTC AGG CGG GAC CGA AGG GAG AAG GAC TAA CCG TAC GTG (SEQ ID NO:12)

...GGG TTC AGG CGG GAC CGA AGG GAG AAG GAC TAA CCG TAC GTG (SEQ ID NO:14)
```

This step generated the plasmid pSS102.

## **Amendments to the Claims**

Please amend claims 1-2 and 22 so as to read as follows:

- 1. method of three-dimensional modeling of a bactericidal/permeability-increasing ("BPI") protein having antimicrobial, lipopolysaccharide-binding, and heparin-binding activities, the method comprising the step of using atomic coordinates of bactericidal/permeability-increasing ("BPI") protein, or fragment, analog or variant thereof, to generate a three-dimensional structural representation of the BPI protein.
- 2. method of three-dimensional modeling bactericidal/permeability-increasing ("BPI") related lipid transfer protein having antimicrobial, lipopolysaccharide-binding, and heparin-binding activities, method comprising the atomic coordinates step of using of bactericidal/permeability-increasing ("BPI") protein, or fragment, analog or variant thereof, to generate a three-dimensional structural representation of the BPIrelated lipid transfer protein.